

73086
JCL

From: Fredman, Jeffrey
Sent: Monday, August 12, 2002 2:31 PM
To: STIC-Biotech/ChemLib
Cc: Angell, Jon E
Subject: FW: Sequence Database Search Request

PLEASE RUSH.

I APPROVE.

Jeff Fredman
(Eric, I got it the second after I called you)

-----Original Message-----

From: Angell, Jon E
Sent: Monday, August 12, 2002 2:31 PM
T : Fredman, Jeffrey
Subject: Sequence Database Search Request

Point of Contact:
Mona Smith
Technical Information Specialist
CM1 6A01
Tel: 308-3278

SEARCH REQUEST FORM

Scientific and Technical Information Center

Examiner# : 78697

Art Unit : 1635

Phone Number: 605-1165

Date: 8/12/02

Serial Number: 09/786,043

Mailbox & Bldg/Room Location: CM1-11E12

Results Format Preferred (circle): Paper

I would like to have a search performed using the following SEQ. ID NOs. from application : 09/786,043

SEQ ID NO. 1-- nucleic acid seq. (<900nucleotides in length)

SEQ ID NO. 2-- amino acid seq. (255 amino acids in length)

NOTE: Please reverse transcribe SEQ ID NO:2 into nucleic acid encoding the seq of SEQ ID NO:2.

I would like a standard search of SEQ ID NO.1 and the cDNA encoding SEQ ID NO:2 , AND an oligomer search of the cDNA encoding SEQ ID NO:2 to identify nucleotide oligos encoding at least 10 contiguous amino acids of SEQ ID NO: 2.

Thanks,
Eric

J. Eric Angell
Art Unit 1635
CM1 12D15
703-605-1165
mailbox CM1 11E12

Searcher: M. Smith
Phone: _____
Location: _____
Date Picked Up: 8/15/02
Date Completed: 8/14/02
Searcher Prep/Review: 10
Clerical: _____
Online time: 15

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 3
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

RECEIVED
TECHNICAL INFORMATION CENTER
(SIC)
AUG 12 2002

DR	InterPro: IPR003118; SAM_PNT.
DR	Pfam: PF00178; Ets; 1.
DR	PFam; PF02198; SAM_PNT; 1.
DR	PRINTS; PR00454; ETS_DOMAIN.
DR	SMART; SM00413; ETS; 1.
DR	PROSITE; PS0061; ETS_DOMAIN; 3; 1.
SO	SEQUENCE 300 AA; 34893 MW; 51CB6E6195E4E06 CRC64;
Query Match	Best Local Similarity 40.7%; Score 574; DB 4; Length 300; Matches 117; Conservative 41.3%; Pred. No. 2. 6e-47; Mismatches 63; Indels 56; Gaps 8;
Qy	22 SWTDLFSNEEYVPAHQPOTACDSWYTSVHPETWKRHWEMLQFCDCDQYKLDTCISPCN 81
Db	23 AWTDSPYCPCNVSSGF---FGSQWHEIHPQWTQKVQWEMLQHLLTNQLDASCIPQE 77
Qy	82 FNIGLQLCSMTOEEFYEAAGCCEYIFILONIRTQG-----YSFENDAEESKA 131
Db	78 FDISGERLCSMSLQEFTTRAAGSAGOLYLSNQHLKINGQCSSDLFOSAHTVKTQTD 120
Qy	132 TIKD-YADSNCL-----KTSGI-----KSQD---C 152
Db	138 SIMTWKEWNLIDTNYGSTVDLDSKFCRAQISMUTSHVVAESPDMKKQDPAAEC 197
Qy	153 PSSRTSDQSSHWEFRDLILSPEENCGILEWEDREGIFRVKSALAKWNGQRKND 212
Db	198 HT-KKHNPRGTHLWEFIRDILNLPDKNPGLIKEDSEGVFRFLKSEAVQWGLKKNNSS 256
Qy	213 RMTYEKLSRALRYYYKIGILEVD-RRLVVKFGKNAHGQEDK 254
Db	257 SMTYEKLSRAMRYYYKREILERVDGRLVVKFGKNAHGRENE 299
RESULT 12	070273
ID	070273
AC	070273;
DT	01-AUG-1998 (TREMBlre. 07, Created) AfcO- 01-JUN-2001 (TREMBlre. 17, Last annotation update)
DT	01-DEC-2001 (TREMBlre. 19, Last annotation update)
DE	EHF.
GN	MUS_musculus (Mouse).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NBII_TAXID=10090;
SEQUENCE FROM N.A.	PTTUEEPIITUTARY; MEDLINE=9862939; PubMed=960089;
RX	Borchert M.A., Kleinbaum L.A., Sun L.Y., Burton F.H.; Molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family. ";
RA	Biocem. Biophys. Res. Commun. 246:176-181(1998).
RT	"
RL	EMBL; AF035527; AAC0119.1; -.
DR	HSSP; Q00422; IAWC.
DR	InterPro; IPR00418; Ets.
DR	InterPro; IPR02341; HSF_ETS.
DR	Pfam; PF00178; Ets; 1.
DR	PRINTS; PR00454; ETS_DOMAIN.
DR	SMART; SM00413; ETS; 1.
DR	PROSITE; PS0061; ETS_DOMAIN; 3; 1.
SO	SEQUENCE 285 AA; 33225 MW; 9138C527C65955F CRC64;
Query Match	Best Local Similarity 36.5%; Score 514; DB 11; Length 285; Matches 112; Conservative 39.7%; Pred. No. 3. 3e-41; Mismatches 64; Indels 69; Gaps 8;
Qy	22 SWTDLFSNEEYVPAHQPOTACDSWYTSVHPETWKRHWEMLQFCDCDQYKLDTCISPCN 81
Db	23 AWTDSPYCPCNVSSGF---FGSQWHEIHPQWTQKVQWEMLQHLLTNQLDASCIPQE 75
Qy	82 FNIGLQLCSMTOEEFYEAAGCCEYIFILONIRTQG-----YSFENDAEESKA 182
Db	76 SMTYEKLSRALRYYYKIGILEVD-RRLVVKFGKNAHGRENE 120
Qy	121 SFENDAE-----SKATIKYADSNCLKTSGI-----KSQD---CHS 154
Db	123 SIMTWKEWNLIDTNYGSTVDLDSKFCRAQISMUTSHVVAESPDMKKQDPHPVKS 183
Qy	155 HSRT-SLOSSHWEFRDLLISPEENCGILEWEDREGIFRVKSALAKWNGQRKND 213
Db	183 HTKHNPRGTHLWEFIRDILNLPDKNPGLIKEDSEGVFRFLKSEAVQWGLKKNNSS 242
Query Match	Similarity 40.3%; Score 568; DB 11; Length 300; Pred. No. 9. 9e-47;

Aug 27, 1998

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 21:21:50 ; Search time 88.19 Seconds
(without alignments)

500.212 Million cell updates/sec
Title: US-09-786-043-2

Perfect score: 1409
Sequence: 1 MLDSVTHSTLPNASFCDPL.....DRRLVYKEFGKNAHGHQEDKL 255

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5622222 seqs, 17294929 residues

total number of hits satisfying chosen parameters:

562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : SPTREMBL_19.*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriopl:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1409	100.0	255	4	095175	095175 homo sapien
2	1409	100.0	265	4	0950Y3	Q9qy3 homo sapien
3	1406	99.8	255	4	Q9RKW5	Q9RKW5 homo sapien
4	1406	99.8	265	4	Q9RKW6	Q9RKW6 homo sapien
5	1338	95.0	253	11	Q921HS	Q921HS mus musculu
6	1330	94.4	253	11	Q922K6	Q922K6 mus musculu
7	587.5	41.8	277	4	Q95V5	Q95V5 homo sapien
8	584.5	41.5	277	4	0950N9	Q950N9 homo sapien
9	578	41.0	300	4	Q95V4	Q95V4 homo sapien
10	574	40.7	300	4	Q95C4	Q95C4 homo sapien
11	574	40.7	300	4	Q9KF9	Q9KF9 homo sapien
12	568	40.3	300	11	09273	09273 mus musculu
13	514.5	36.5	285	11	099k12	099k12 mus musculu
14	430.5	30.6	371	11	05275	05275 mus musculu
15	427.5	30.3	348	4	Q9718	Q9718 homo sapien
16	422	30.0	371	4	P78545	P78545 homo sapien

Query Match 100.0%; Score 1409; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 6.1e-128; Mismatches 0; Indels 0; Gaps 0;

SEQUENCE FROM N.A. [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99054671; PubMed-9840936;
RA Zhou J., Ng A.Y., Tymms M.J., Jermini L.S., Seth A.K., Thomas R.S., Kola I.;
RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of ETS genes and maps to human chromosome 11p13-15, a region subject to LOH and rearrangement in human carcinoma cell lines." [2]
RL Oncogene 17:2719-2732(1998). [3]
DR EMBL: AR04973; AAC79755; 1.
DR HSSP; Q00422; 1AWC.
DR InterPro: IPR000418; Ets.
DR InterPro: IPR00241; HSF_ETS.
DR InterPro: IPR003118; SAM_PNT.
DR Pfam: PF00118; Ets; 1.
DR Pfam: PF02198; SAM_PNT; 1.
DR PRINTS; PRO0454; ETSDORAIN.
DR SMART; SM00413; Ets; 1..
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PSS0061; ETS_DOMAIN; 1.
SQ SEQUENCE 255 AA; 30121 MW; AE611C5B178ECB555 CRC64;

RA	Akbarali Y., Finger E., Boltax J., Endress G., Munger K., Kunsch C., Libermann T.A.; "Characterization of ESE-2, a novel ESE-1-related Ets transcription factor that is restricted to glandular epithelium and differentiated keratinocytes.";	Qy	61 EWLOFCCDQYKLDTNCISFCNFNISGLQLCSTMQEVEAAGCGEYLYPILONIRTOGY 120
RT		Db	61 EWLOFCCDQYKLDTNCISFCNFNISGLQLCSTMQEVEAAGCGEYLYPILONIRTOGY 120
RT		Qy	121 SFENDAESKATIKDYADSNCNLTKSGIKSQQDCHSHRSSTSLOSSHLWEFVDRLLSPPEENC 180
RL	J. Biol. Chem. 274:29439-29452 (1999).	Db	121 SFENDAESKATIKDYADSNCNLTKSGIKSQQDCHSHRSSTSLOSSHLWEFVDRLLSPPEENC 178
DR	EMBL; AP1540.; ADD2960.1; -.	Qy	181 GILEWEDREQGIFRVKSEALAKMWRKNDRTMYEKLSRALYYKTGILERDRRLV 240
DR	HSSP; Q00422; IANC.	Db	179 GILEWEDREQGIFRVKSEALAKMWRKNDRTMYEKLSRALYYKTGILERDRRLV 238
DR	InterPro; IPRO000418; ETS.	Qy	241 YKEGKNAHGWQEDKL 255
DR	InterPro; IPRO02341; HSF-ETS.	Db	239 YKEGKNAHGWQEEKL 253
DR	InterPro; IPRO003118; SAM_PNT.		
DR	Pfam; PF00178; ETS; 1.		
DR	Pfam; PF02198; SAM_PNT; 1.		
DR	PRINTS; PR00054; ETS DOMAIN.		
DR	SMART; SM00413; ETS; 1.		
DR	SMART; SM00231; SAM_PNT; 1.		
DR	PROSITE; PS50061; ETS DOMAIN 3; 1.		
SQ	SEQUENCE . 265 AA; 31295 MW; B2921A79A45768E3 CRC64;	RESULT 6	
		0923K6	
		ID Q922K6 PRELIMINARY;	
		AC Q922K6;	
		DT 01-MAY-1999 (TREMBrel. 10; Created)	
		DT 01-MAY-1999 (TREMBrel. 10; Last sequence update)	
		DT 01-DEC-2001 (TREMBrel. 19; Last annotation update)	
		DE E74-LIKE FACTOR 5.	
		GN ELF5.	
		OS Mus musculus (Mouse).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.	
		NCBI_TAXID=10090;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RX PMID=99054671; PubMed=9840936;	
		RA Zhou J., Ng A.Y., Tytms M.J., Jermin L.S., Seth A.K., Thomas R.S., Kola I.;	
		RA RT A novel transcription factor, BLF5, belongs to the ELF subfamily of RT ETS genes and maps to human chromosome 11p13-15, a region subject to RT LOH and rearrangement in human carcinoma cell lines.";	
		RL Oncogene 17:2719-2732 (1998).	
		DR EMBL; AR049702; AAC79754.1; -.	
		DR HSSP; Q00422; IANC.	
		DR MGDB; MGDB:1335079; Elfs.	
		DR InterPro; IPR000418; Ets.	
		DR InterPro; IPR0241; HSF_ETS.	
		DR InterPro; IPR003118; SAM_PNT.	
		DR Pfam; PF00178; Ets; 1.	
		DR Pfam; PF02198; SAM_PNT; 1.	
		DR PRINTS; PR00054; ETS DOMAIN.	
		DR SMART; SM00413; ETS; 1.	
		DR SMART; SM0051; SAM_PNT; 1.	
		DR PROSITE; PS50061; ETS DOMAIN 3; 1.	
		SQ SEQUENCE . 253 AA; 29971 MW; 3FD028DA77AFCE48 CRC48;	
		RESULT 5	
		0921HS5	
		ID Q921HS5 PRELIMINARY;	
		AC Q921HS5;	
		DT 01-DEC-2001 (TREMBrel. 19; Created)	
		DT 01-DEC-2001 (TREMBrel. 19; Last sequence update)	
		DT 01-DEC-2001 (TREMBrel. 19; Last annotation update)	
		DE SIMILAR TO E74-LIKE FACTOR 5.	
		OS Mus musculus (Mouse).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.	
		NCBI_TAXID=10090;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RA Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.	
		DR EMBL; BC012424; AAH12424.1; -.	
SQ	SEQUENCE . 253 AA; 29872 MW;	3FC4799F77AFCF48 CRC64;	
		Query Match 95.0%; Score 1338; DB 11; Length 253;	
		Best Local Similarity 94.5%; Pred. No. 4..2e-121;	
		Matches 241; Conservative 8; Mismatches 14; Indels 2; Gaps 1;	
		DB 1 MD5VTHSTFLPNASCDPLMSWTDLSNEEYPAFHOTACDSYNTSVHPEYWTKRHW 60	
		Qy 1 MD5VTHSTFLPNASCDPLMSWTDLSNEEYPAFHOTACDSYNTSVHPEYWTKRHW 60	
		Db 1 MD5VTHSTFLPNASECDPLMPWTDLSNEDYYPAFHOTACDSYNTSVHPEYWTKRHW 60	
		Qy 1 MD5VTHSTFLPNASCDPLMSWTDLSNEEYPAFHOTACDSYNTSVHPEYWTKRHW 60	
		Db 179 GILEWEDREQGIFRVKSEALAKMWRKNDRTMYEKLSRALYYKTGILERDRRLV 238	

RT ESE-1.";	RP SEQUENCE FROM N.A.
RL J. Biol. Chem. 275:2986-2998(2000).	RA Mitchell S.C., Levin E., Hubert R., Yeramian C., Saffran D.C., Afar D.E.H.; RT "Up-Regulation of the Epithelial-Specific Transcription Factor Genes hESF and ESX in Advanced prostate Cancer.";
DR EMBL; AF124439; AAC30991.1; -;	RT heSF and ESX in Advanced prostate Cancer.";
DR HSSP; Q00422; IAWC.	RT
DR InterPro; IPR000418; Ets.	RT Prostate 0:0-0.1999;
DR InterPro; IPR002341; HSF_ETS.	DR DR AF212848; AAC51670.1;
DR InterPro; IPR001118; SAM_PNT.	DR DR AF157552; CAC1701.1;
DR Pfam; PF00178; Ets; 1.	DR DR AF03977; AAC35644.1;
DR PRINTS; PRO0454; ETS_DOMAIN.	DR DR HSSP; Q000422; IAWC.
DR SMART; SM00413; Ets; 1.	DR DR InterPro; IPR00418; Ets.
DR SMART; SM00251; SAM_PNT; 1.	DR DR InterPro; IPR003118; HSF_ETS.
DR PROSITE; PS50061; ETS_DOMAIN_3; 1.	DR DR InterPro; IPR003118; SAM_PNT.
SEQUENCE 300 AA; 34920 MW; 3DEC66577780FEC1 CRC64;	DR DR Pfam; PF00178; Ets; 1.
	DR DR PF02198; SAM_PNT; 1.
	DR DR PRINTS; PRO0454; ETS_DOMAIN.
	DR DR SMART; SM00413; Ets; 1.
	DR DR SMART; SM00251; SAM_PNT; 1.
	DR DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
	SEQUENCE 300 AA; 34892 MW; 5CABB38BAF852ED0 CRC64;
Query Match 41.0%; Score 578; DB 4; Length 300;	Query Match 40.7%; Score 574; DB 4; Length 300;
Best Local Similarity 41.7%; Pred. No. 1.1e-47;	Best Local Similarity 41.3%; Pred. No. 2.8e-47;
Matches 118; Conservative 47; Mismatches 62;	Matches 117; Conservative 47; Mismatches 63;
Indels 56; Gaps 8;	Indels 56; Gaps 8;
Db 22 SMTDLSNEEYYPAFEHOTACDSYWTWSHPEWTKRHYWEWLOFCDCOYKLDTNICFCN 81	Db 22 SMTDLSNEEYYPAFEHOTACDSYWTWSHPEWTKRHYWEWLOFCDCQKYKUDTNICFCN 81
Db 23 AWTDYSYSTCNVSGF ----FGSQWHEIHPQWTKYQWEWLNQLHLDTNOLANCIFQE 77	Db 23 AWTDYSYSTCNVSGF ----FGSQWHEIHPQWTKYQWEWLNQLHLDTNOLANCIFQE 77
Qy 82 FNTISGLQCSMTOBEFYEAAGLGEYLFLONIRTG -----YSFFNDAAEBSKA 131	Qy 82 FNTISGLQCSMTOBEFYEAAGLGEYLFLONIRTG -----YSFFNDAAEBSKA 131
Db 78 FDINGENICCSMSLQEFTRAAGTAGQOLLYSNQHLKWNGQCSSLDFQSTHNVIKTEQTEP 137	Db 78 FDINGEHLCMSLQEFTRAAGTAGQOLLYSNQHLKWNGQCSSLDFQSTHNVIKTEQTEP 137
Qy 132 TIKD-YADSNCI-----KTSGI-----C 152	Qy 132 TIKD-YADSNCI-----KTSGI-----C 152
Db 138 SIMNTWDENLYDNTNNGSTVLLDGKTFCRVQISMTTSHLPVAESPDMKKEQDPACK 197	Db 138 SIMNTWDENLYDNTNNGSTVLLDGKTFCRVQISMTTSHLPVAESPDMKKEQDPACK 197
Qy 153 HSHSRSTSLOSSHLWEFYRDLLSPENCNGILEMEDREQIFRVVKSEBALAKWQQRKKND 212	Qy 153 HSHSRSTSLOSSHLWEFYRDLLSPENCNGILEMEDREQIFRVVKSEBALAKWQQRKKND 212
Db 198 HF-KHNPRGFTLWEFTDILLNPDKNGPLGLKWEDEREGVFRFLKSEAVAQLWGKKNN 256	Db 198 HF-KHNPRGFTLWEFTDILLNPDKNGPLGLKWEDEREGVFRFLKSEAVAQLWGKKNN 256
Qy 213 RMYEKUSRALRYYYKGILERD-RFLVYKGKGNAHGQWEKD 254	Qy 213 RMYEKUSRALRYYYKGILERD-RFLVYKGKGNAHGQWEKD 254
Db 257 SMTYEKUSRAMYYKKREILLEVDGRLVYKGKGNAHGWRNE 299	Db 257 SMTYEKUSRAMYYKKREILLEVDGRLVYKGKGNAHGWRNE 299
RESULT 10	RESULT 11
Q9NZC4 ID PRELIMINARY; PRT; 300 AA.	Q9UKF9 ID PRELIMINARY; PRT; 300 AA.
AC Q9NZC4; PRT; 300 AA.	AC Q9UKF9; PRT; 300 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)	DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ETS DOMAIN TRANSCRIPTION FACTOR (DJ8/5K15.1.2).	DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
GN Homo sapiens (Human)	DE ETS_HOMOLOGOUS_FACTOR.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	GN EHF.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TAXID9606;	RN [1] -
RN [1]	RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RA Brooks Wilson A.R., Buckler A., Cardon L., Carey A.H., Galvin M., Miller A., North M., Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RA Kleinbaum L.A., Duggan C., Ferreira E., Buttice G., Burton F.H.; RT "Human chromosomal localization, tissue/tumor expression, and regulatory function of the ets family gene EHF"; RL Biochem. Biophys. Res. Commun. 264:119-126 (1999). DR EMBL; AF170583; AAC05998.1; DR HSSP; Q00422; IAWC.
RA Mushegian A., Carlee L., Watanakul T., Chu S., McCormick M.K.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.	DR InterPro; IPR000418; Ets.
RA Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.	DR InterPro; IPR002341; HSF_ETS.
RN [4]	RN [1]

Qy 214 MTYEKLRSRALRYYKTTGILERVD-RRLVYKFGKNAHGQWEDK 254
 Db 243 MTYEKLRSRALRYYKTTGILERVDGRRVYKFGKNAHGQWENE 284

RESULT 14

ID 035275 PRELIMINARY; PRT; 371 AA.

AC 035275; DE 01-JAN-1998 (TMBMLrel. 05, Created)
 DT 01-JAN-1998 (TMBMLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TMBMLrel. 19, Last annotation update)

DE ETS TRANSCRIPTION FACTOR.

GN ELF3 OR ERF3.

OS Mus musculus (Mouse).

OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LUNG;

RX MEDLINE="9055619; PubMed=9395341; Pubmed_id=9395341; RA Tymms M.J., Ng A.Y., Thomas R.S., Schutte B.C., Zhou J., Eyre H.J., RA Sutherland G.R., Seth A., Rosenberg M., Papas T., Debonck C., Kola I.; RT "A novel epithelial-expressed Ets gene, ELF3: human and murine cDNA sequences, murine genomic organization, human mapping to 1q32.2 and expression in tissues and cancer."; RT Oncogene 15:2449-2452(1997); RI AF06294; AAB6585.1; -.

DR HSSP; P28324; IBC8.

DR MGD; MGI:1101781; Eif3.

DR InterPro; IPR00637; AT_hook.

DR InterPro; IPR00418; Ets.

DR InterPro; IPR00234; HSP_ETS.

DR InterPro; IPR00318; SAM_PNT.

DR Pfam; PF02178; AT_hook; 1.

DR Pfam; PF00178; Ets; 1.

DR Pfam; PF0198; SAM_PNT; 1.

DR PRINTS; PRO0454; ETSDOMAIN.

DR SMART; SM00384; AT_hook; 1.

DR SMART; SM00413; ETS; 1.

DR SMART; SM00251; SAM_PNT; 1.

DR PROSITE; PS50061; ETS_DOMAIN_3; 1.

SEQ SEQUENCE 371 AA; 42060 MW; 042EDACC05839EE6 CRC64;

Query Match Score 430.5; DB 11; Length 371;
 Best Local Similarity 30.7%; Fred. No. 2.4e-33;
 Matches 95; Conservative 47; Mismatches 68; Indels 99; Gaps 7;

Qy 46 WTSVHPEYWKRVHVVNEWLQFCDOYKVLDTNCISPCNFNTISGLQCSMTQEVEAGLCG 105
 Db 58 WTSEPOFWSKTQVLEWISQVERKYDASSIDEFSICDMGATLSCALEBLRLVFGPLG 117

Qy 106 EYLY-----FILQNTRQYSF-----FNDAEESK 130
 Db 118 DQLHAQRDLTSNSSDELWSWIELKEDGNSFQESIGDGSFPDQGSPEAQELLDGROAS 177

Qy 131 -----ATIK-----DYADSNCIQTSGIKSQ-- 150
 Db 178 PYYCSTYGPAPSPGSSDVSTARATPQSSHASDGGSDYDLDLTISKVPRDGPDYKK 237

Qy 151 -----DC--HSHSRSTSLOSSHILWEPYRDLILSPPEENCGILEWED 187
 Db 238 GEPKIGKRKRGPRPLSKSKEYWDCLGSKSKXPAHGPRLWIFRDLLIHPNELNEGAMKWEN 297

Qy 188 REQGFRRVKVSEALKMKGQKKNDRMYEKLSLALRYYKTTGILERVD-RRLVYKFGK 246
 Db 298 RHEGFKELSEAVALQWGQKKSMMTYEKLSRAMYKZKREILLERVGRLVYKFGK 357

Qy 247 AHGQEDKL 255
 Db 358 SSGWKEEV 366

RESULT 15

ID 039718 PRELIMINARY; PRT; 348 AA.

AC 039718; DE 01-MAY-1997 (TMBMLrel. 03, Created)
 DT 01-MAY-1997 (TMBMLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TMBMLrel. 17, Last annotation update)

DE EPITHELIAL-SPECIFIC TRANSCRIPTION FACTOR ESE-1A.

GN ESE-1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER, AND PANCREATIC CARCINOMA;

RX MEDLINE="97378019; PubMed=2334760; Oettgen P., Alain R.M., Barcinski M.A., Brown L., Akbarali Y., RA Boltax J., Kunsch C., Munger K., Libermann T.A.; RT "Isolation and characterization of a novel epithelium-specific transcription factor, ESE-1, a member of the ets family."; RL Mol. Cell. Biol. 17:419-4433(1997); DR EMBL; U73844; AB265894.1; HSSP; P28324; IBC8. DR InterPro; IPR00637; AT_hook. DR InterPro; IPR00418; Ets. DR InterPro; IPR00341; HSF-ETS. DR InterPro; IPR003118; SAM_PNT. DR Pfam; PF00178; Ets; 1. DR Pfam; PF02198; SAM_PNT; 1. DR PRINTS; PRO034; ETSDOMAIN. DR SMART; SM00384; AT_hook; 1. DR SMART; SM00413; ETS; 1. DR SMART; SM00251; SAM_PNT; 1. DR PROSITE; PS50061; ETS_DOMAIN_3; 1. SQ SEQUENCE 348 AA; 39357 MW; AE2A633633CA305E CRC64;

Query Match Score 30.3%; DB 4; Length 348;
 Best Local Similarity 31.0%; Fred. No. 4.3e-33; Mismatches 49; Indels 79; Gaps 5;

Qy 46 WTSVHPEYWKRVHVVNEWLQFCDOYKVLDTNCISPCNFNTISGLQCSMTQEVEAGLCG 105
 Db 59 WIGEQPFWSKTLWISQYEVKNYDASSIDEFSICDMGATLSCALEBLRLVFGPLG 118

Qy 106 EVLYFLQNI-----QGKFSEFDNBESAKI-- 133
 Db 119 DQLHAQRDLTSNSSDELWSWIELKEDGNSFQESIGDGSFPDQGSPEAQELLDGYSTAGT 178

Qy 134 -----KDYADSNCLNLTKTSGIKSQDCH----- 153
 Db 179 GASRSSHSSDGSGYDLDPPDKLPSDGR--DCKRGDPKHGKKRGRKLKEYWD 236

Qy 154 -----SHSRSTSLOSSHILWEPYRDLILSPPEENCGILEWED 209
 Db 237 CLEGKSKHAFRGTHLWEFIRDLLIHPNELNEGAMKWENRHGVFKPLRSEAVOLQGOKK 296

Qy 210 KNDRMYTEKLSLALRYYKTTGILERVD-RRLVYKFGKNAHGWQEDKL 255
 Db 297 KNSWVTEKLSRAMYKZKREILLERVGRLVYKFGKNSGWKEEV 343

Search completed: August 13, 2002, 21:31:15
 Job time: 565 sec

